

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

WARREN, Patrick V.

SWANSON, Ronald V.

(ii) TITLE OF INVENTION:

TRANSAMINASES AND AMINOTRANSFERASES

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN

(B) STREET: 6 BECKER FARM ROAD

(C) CITY: ROSELAND

(D) STATE: NEW JERSEY

(E) COUNTRY: USA

(F) ZIP: 07068

(v)

COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 INCH DISKETTE

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: WORD PERFECT 5.1

(vi)

CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unassigned

(B) FILING DATE: Concurrently

(C) CLASSIFICATION: Unassigned

(vii)

PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii)

ATTORNEY/AGENT INFORMATION:

(A) NAME: HERRON, CHARLES J.

(B) REGISTRATION NUMBER: 28,019

(C) REFERENCE/DOCKET NUMBER: 331400-38

(ix)

TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700

(B) TELEFAX: 201-994-1744

(2)

INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 52 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGATTGAA GACCCTATGG AC

52

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGATCT TTAAGCACTT CTCTCAGGTT C

31

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGGACAGG CTTGAAAAAG TA

52

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGATCT TCAGCTAAGC TTCTCTAAGA A

31

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGTGGGAA TTAGACCCTA AA

52

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAGGATCC CTACACCTGT TTTTCAAGCT C

31

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGACATAC TTAATGAACA AT

52

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGAAGATCT TTATGAGAAG TCCCTTTCAA G

31

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGCGGAAA CTGGCCGAGC GG

52

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

31

CGGAGGATCC TTAAAGTGCC GCTTCGATCA A

- (2) INFORMATION FOR SEQ ID NO:11:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

52

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGTGCGGG ATAGTCGGAT AC

- (2) INFORMATION FOR SEQ ID NO:12:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

31

CGGAAGATCT TTATTCCACC GTGACCGTTT T

- (2) INFORMATION FOR SEQ ID NO:13:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

52

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGATACCC CAGAGGATTA AG

- (2) INFORMATION FOR SEQ ID NO:14:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

31

CGGAAGATCT TTAAAGAGAG CTTGAAAGGG A

- (2) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

52

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAAGCCG TACGCTAAAT AT

- (2) INFORMATION FOR SEQ ID NO:16:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

31

CGGAAGATCT CTAATACACA GGAGTGATCC A

- (2) INFORMATION FOR SEQ ID NO:17:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 1245 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG ATT GAA GAC CCT ATG GAC TGG GCT TTT CCG AGG ATA AAG AGA CTG 48
Met Ile Glu Asp Pro Met Asp Trp Ala Phe Pro Arg Ile Lys Arg Leu 15

CCT CAG TAT GTC TTC TCT CTC GTT AAC GAA CTC AAG TAC AAG CTA AGG 96
Pro Gln Tyr Val Phe Ser Leu Val Asn Glu Leu Lys Tyr Lys Leu Arg 30

CGT GAA GGC GAA GAT GTA GTG GAT CTT GGT ATG GGC AAT CCT AAC ATG 144
Arg Glu Gly Glu Asp Val Val Leu Gly Met Gly Asn Pro Asn Met 45

CCT CCA GCA AAG CAC ATA ATA GAT AAA CTC TGC GAA GTG GCT CAA AAG 192
Pro Pro Ala Lys His Ile Ile Asp Lys Leu Cys Glu Val Ala Gln Lys 60

CCG AAC GTT CAC GGA TAT TCT GCG TCA AGG GGC ATA CCA AGA CTG AGA Pro Asn Val His Gly Tyr Ser Ala Ser Arg Gly Ile Pro Arg Leu Arg 65 70 75 80	240
AAG GCT ATA TGT AAC TTC TAC GAA GAA AGG TAC GGA GTG AAA CTC GAC Lys Ala Ile Cys Asn Phe Tyr Glu Glu Arg Tyr Gly Val Lys Leu Asp 85 90 95	288
CCT GAG AGG GAG GCT ATA CTA ACA ATC GGT GCA AAG GAA GGG TAT TCT Pro Glu Arg Glu Ala Ile Leu Thr Ile Gly Ala Lys Glu Gly Tyr Ser 100 105 110	336
CAT TTG ATG CTT GCG ATG ATA TCT CCG GGT GAT ACG GTA ATA GTT CCT His Leu Met Leu Ala Met Ile Ser Pro Gly Asp Thr Val Ile Val Pro 115 120 125	384
AAT CCC ACC TAT CCT ATT CAC TAT TAC GCT CCC ATA ATT GCA GGA GGG Asn Pro Thr Tyr Pro Ile His Tyr Tyr Ala Pro Ile Ile Ala Gly Gly 130 135 140	432
GAA GTT CAC TCA ATA CCC CTT AAC TTC TCG GAC GAT CAA GAT CAT CAG Glu Val His Ser Ile Pro Leu Asn Phe Ser Asp Asp Gln Asp His Gln 145 150 155 160	480
GAA GAG TTT TTA AGG AGG CTT TAC GAG ATA GTA AAA ACC GCG ATG CCA Glu Glu Phe Leu Arg Arg Leu Tyr Glu Ile Val Lys Thr Ala Met Pro 165 170 175	528
AAA CCC AAG GCT GTC GTC ATA AGC TTT CCT CAC AAT CCA ACG ACC ATA Lys Pro Lys Ala Val Val Ile Ser Phe Pro His Asn Pro Thr Thr Ile 180 185 190	576
ACG GTA GAA AAG GAC TTT TTT AAA GAA ATA GTT AAG TTT GCA AAG GAA Thr Val Glu Lys Asp Phe Phe Lys Glu Ile Val Lys Phe Ala Lys Glu 195 200 205	624
CAC GGT CTC TGG ATA ATA CAC GAT TTT GCG TAT GCG GAT ATA GCC TTT His Gly Leu Trp Ile Ile His Asp Phe Ala Tyr Ala Asp Ile Ala Phe 210 215 220	672
GAC GGT TAC AAG CCC CCC TCA ATA CTC GAA ATA GAA GGT GCT AAA GAC Asp Gly Tyr Lys Pro Pro Ser Ile Leu Glu Ile Glu Gly Ala Lys Asp 225 230 235 240	720
GTT GCG GTT GAG CTC TAC TCC ATG TCA AAG GGC TTT TCA ATG GCG GGC Val Ala Val Glu Leu Tyr Ser Met Ser Lys Gly Phe Ser Met Ala Gly 245 250 255	768
TGG AGG GTA GCC TTT GTC GTT GGA AAC GAA ATA CTC ATA AAA AAC CTT Trp Arg Val Ala Phe Val Val Gly Asn Glu Ile Leu Ile Lys Asn Leu 260 265 270	816
GCA CAC CTC AAA AGC TAC TTG GAT TAC GGT ATA TTT ACT CCC ATA CAG Ala His Leu Lys Ser Tyr Leu Asp Tyr Gly Ile Phe Thr Pro Ile Gln 275 280 285	864
GTG GCC TCT ATT ATC GCA TTA GAG AGC CCC TAC GAA ATC GTG GAA AAA Val Ala Ser Ile Ile Ala Leu Glu Ser Pro Tyr Glu Ile Val Glu Lys 290 295 300	912
ACC GCA AAG GTT TAC CAA AAA AGA AGA GAC GTT CTG GTG GAA GGG TTA	960

Thr	Ala	Lys	Val	Tyr	Gln	Lys	Arg	Arg	Asp	Val	Leu	Val	Glu	Gly	Leu	320	
305					310					315							
AAC	AGG	CTC	GGC	TGG	AAA	GTA	AAA	AAA	CCT	AAG	GCT	ACC	ATG	TTC	GTC		1008
Asn	Arg	Leu	Gly	Trp	Lys	Val	Lys	Lys	Pro	Lys	Ala	Thr	Met	Phe	Val		
					325				330					335			
TGG	GCA	AAG	ATT	CCC	GAA	TGG	ATA	AAT	ATG	AAC	TCT	CTG	GAC	TTT	TCC		1056
Trp	Ala	Lys	Ile	Pro	Glu	Trp	Ile	Asn	Met	Asn	Ser	Leu	Asp	Phe	Ser		
				340				345					350				
TTG	TTC	CTC	CTA	AAA	GAG	GCG	AAG	GTT	GCG	GTA	TCC	CCG	GGT	GTG	GGC		1104
Leu	Phe	Leu	Leu	Lys	Glu	Ala	Lys	Val	Ala	Val	Ser	Pro	Gly	Val	Gly		
				355			360					365					
TTT	GGT	CAG	TAC	GGA	GAG	GGG	TAC	GTA	AGG	TTT	GCA	CTT	GTA	GAA	AAT		1152
Phe	Gly	Gln	Tyr	Gly	Glu	Gly	Tyr	Val	Arg	Phe	Ala	Leu	Val	Glu	Asn		
				370			375				380						
GAA	CAC	AGG	ATC	AGA	CAG	GCT	ATA	AGG	GGA	ATA	AGG	AAA	GCC	TTC	AGA		1200
Glu	His	Arg	Ile	Arg	Gln	Ala	Ile	Arg	Gly	Ile	Arg	Lys	Ala	Phe	Arg		
					385		390			395				400			
AAA	CTC	CAG	AAG	GAG	AGG	AAA	CTT	GAA	CCT	GAG	AGA	AGT	GCT	TAA			1245
Lys	Leu	Gln	Lys	Glu	Arg	Lys	Leu	Glu	Pro	Glu	Arg	Ser	Ala	End			
				405				410				414					

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1122 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG	GAC	AGG	CTT	GAA	AAA	GTA	TCA	CCC	TTC	ATA	GTA	ATG	GAT	ATC	CTA	48
Met	Asp	Arg	Leu	Glu	Lys	Val	Ser	Pro	Phe	Ile	Val	Met	Asp	Ile	Leu	
				5				10						15		
GCT	CAG	GCC	CAG	AAG	TAC	GAA	GAC	GTA	GTA	CAC	ATG	GAG	ATA	GGA	GAG	96
Ala	Gln	Ala	Gln	Lys	Tyr	Glu	Asp	Val	Val	His	Met	Glu	Ile	Gly	Glu	
				20			25					30				
CCC	GAT	TTA	GAA	CCG	TCT	CCC	AAG	GTA	ATG	GAA	GCT	CTG	GAA	CGT	GCG	144
Pro	Asp	Leu	Glu	Pro	Ser	Pro	Lys	Val	Met	Glu	Ala	Leu	Glu	Arg	Ala	
			35				40				45					
GTG	AAG	GAA	AAG	ACG	TTC	TTC	TAC	ACC	CCT	GCT	CTG	GGA	CTC	TGG	GAA	192
Val	Lys	Glu	Lys	Thr	Phe	Phe	Tyr	Thr	Pro	Ala	Leu	Gly	Leu	Trp	Glu	
			50			55			60							
CTC	AGG	GAA	AGG	ATA	TCG	GAG	TTT	TAC	AGG	AAA	AAG	TAC	AGC	GTT	GAA	240
Leu	Arg	Glu	Arg	Ile	Ser	Glu	Phe	Tyr	Arg	Lys	Lys	Tyr	Ser	Val	Glu	
				65		70			75			80				
GTT	TCT	CCA	GAG	AGA	GTC	ATC	GTA	ACT	ACC	GGA	ACT	TCG	GGA	GCG	TTT	288
Val	Ser	Pro	Glu	Arg	Val	Ile	Val	Thr	Thr	Gly	Thr	Ser	Gly	Ala	Phe	
					85			90				95				
CTC	GTA	GCC	TAC	GCC	GTA	ACA	CTA	AAT	GCG	GGA	GAG	AAG	ATA	ATC	CTC	336

Leu Val Ala Tyr Ala Val Thr Leu Asn Ala Gly Glu Lys Ile Ile Leu
 100 105 110

CCA GAC CCC TCT TAC CCC TGT TAC AAA AAC TTT GCC TAC CTC TTA GAC 384
 Pro Asp Pro Ser Tyr Pro Cys Tyr Lys Asn Phe Ala Tyr Leu Leu Asp
 115 120 125

GCT CAG CCG GTT TTC GTA AAC GTT GAC AAG GAA ACG AAT TAC GAA GTA 432
 Ala Gln Pro Val Phe Val Asn Val Asp Lys Glu Thr Asn Tyr Glu Val
 130 135 140

AGG AAA GAG ATG ATA GAA GAC ATT GAT GCG AAA GCC CTT CAC ATT TCC 480
 Arg Lys Glu Met Ile Glu Asp Ile Asp Ala Lys Ala Leu His Ile Ser
 145 150 155 160

TCG CCT CAA AAC CCT ACG GGC ACA CTC TAC TCA CCT GAA ACC CTG AAG 528
 Ser Pro Gln Asn Pro Thr Gly Thr Leu Tyr Ser Pro Glu Thr Leu Lys
 165 170 175

GAA CTT GCG GAG TAC TGC GAA GAG AAG GGT ATG TAC TTC ATA TCC GAC 576
 Glu Leu Ala Glu Tyr Cys Glu Glu Lys Gly Met Tyr Phe Ile Ser Asp
 180 185 190

GAG ATT TAC CAC GGA CTC GTT TAC GAA GGT AGG GAG CAC ACA GCA CTT 624
 Glu Ile Tyr His Gly Leu Val Tyr Glu Gly Arg Glu His Thr Ala Leu
 195 200 205

GAG TTC TCT GAC AGG GCT ATT GTC ATA AAC GGG TTT TCT AAG TAC TTC 672
 Glu Phe Ser Asp Arg Ala Ile Val Ile Asn Gly Phe Ser Lys Tyr Phe
 210 215 220

TGT ATG CCA GGT TTC AGG ATA GGG TGG ATG ATA GTT CCG GAA GAA CTC 720
 Cys Met Pro Gly Phe Arg Ile Gly Trp Met Ile Val Pro Glu Glu Leu
 225 230 235 240

GTG AGA AAG GCG GAA ATA GTA ATT CAG AAC GTA TTT ATA TCT GCC CCG 768
 Val Arg Lys Ala Glu Ile Val Ile Gln Asn Val Phe Ile Ser Ala Pro
 245 250 255

ACG CTC AGT CAG TAC GCC GCC CTT GAG GCT TTT GAT TAC GAG TAT TTG 816
 Thr Leu Ser Gln Tyr Ala Ala Leu Glu Ala Phe Asp Tyr Glu Tyr Leu
 260 265 270

GAG AAG GTA AGA AAA ACC TTT GAA GAG AGG AGG AAC TTC CTT TAT GGG 864
 Glu Lys Val Arg Lys Thr Phe Glu Glu Arg Arg Asn Phe Leu Tyr Gly
 275 280 285

GAA CTG AAA AAA CTC TTC AAG ATA GAC GCG AAA CCT CAG GGA GCT TTT 912
 Glu Leu Lys Lys Leu Phe Lys Ile Asp Ala Lys Pro Gln Gly Ala Phe
 290 295 300

TAC GTA TGG GCA AAC ATA AGT GAT TAC TCC ACA GAT AGC TAC GAA TTT 960
 Tyr Val Trp Ala Asn Ile Ser Asp Tyr Ser Thr Asp Ser Tyr Glu Phe
 305 310 315 320

GCT TTA AAA CTT TTA AGG GAG GCG AGG GTG GCG GTA ACG CCC GGG GTG 1008
 Ala Leu Lys Leu Leu Arg Glu Ala Arg Val Ala Val Thr Pro Gly Val
 325 330 335

GAC TTT GGA AAA AAC AAA ACG AAG GAG TAT ATA AGG TTT GCT TAT ACG 1056
 Asp Phe Gly Lys Asn Lys Thr Lys Glu Tyr Ile Arg Phe Ala Tyr Thr
 340 345 350

AGA AAG ATA GAA GAA CTT AAG GAG GGC GTT GAA AGG ATA AAG AAG TTC
 Arg Lys Ile Glu Glu Leu Lys Glu Gly Val Glu Arg Ile Lys Lys Phe
 355 360 365

1104

TTA GAG AAG CTT AGC TGA
 Leu Glu Lys Leu Ser End
 370

1122

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1359 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG TGG GAA TTA GAC CCT AAA ACG CTC GAA AAG TGG GAC AAG GAG TAC
 Met Trp Glu Leu Asp Pro Lys Thr Leu Glu Lys Trp Asp Lys Glu Tyr
 5 10 15

48

TTC TGG CAT CCA TTT ACC CAG ATG AAA GTC TAC AGA GAA GAA GAA AAC
 Phe Trp His Pro Phe Thr Gln Met Lys Val Tyr Arg Glu Glu Glu Asn
 20 25 30

96

CTG ATA TTT GAA CGC GGA GAA GGC GTT TAC CTG TGG GAC ATA TAC GGC
 Leu Ile Phe Glu Arg Gly Glu Gly Val Tyr Leu Trp Asp Ile Tyr Gly
 35 40 45

144

AGG AAG TAT ATA GAT GCC ATA TCT TCC CTC TGG TGC AAC GTC CAC GGA
 Arg Lys Tyr Ile Asp Ala Ile Ser Ser Leu Trp Cys Asn Val His Gly
 50 55 60

192

CAT AAC CAC CCT AAA CTG AAC AAC GCA GTT ATG AAA CAG CTC TGT AAG
 His Asn His Pro Lys Leu Asn Asn Ala Val Met Lys Gln Leu Cys Lys
 65 70 75 80

240

GTA GCT CAC ACA ACT ACT CTG GGA AGT TCC AAC GTT CCC GCC ATA CTC
 Val Ala His Thr Thr Thr Leu Gly Ser Ser Asn Val Pro Ala Ile Leu
 85 90 95

288

CTT GCA AAG AAG CTT GTA GAA ATT TCT CCT GAA GGA TTA AAC AAG GTC
 Leu Ala Lys Lys Leu Val Glu Ile Ser Pro Glu Gly Leu Asn Lys Val
 100 105 110

336

TTT TAC TCC GAA GAC GGT GCG GAA GCA GTA GAG ATA GCG ATA AAG ATG
 Phe Tyr Ser Glu Asp Gly Ala Glu Ala Val Glu Ile Ala Ile Lys Met
 115 120 125

384

GCT TAT CAC TAC TGG AAG AAC AAG GGA GTT AAA GGG AAA AAC GTT TTC
 Ala Tyr His Tyr Trp Lys Asn Lys Gly Val Lys Gly Lys Asn Val Phe
 130 135 140

432

ATA ACG CTT TCC GAA GCC TAC CAC GGG GAT ACT GTA GGA GCG GTT AGC
 Ile Thr Leu Ser Glu Ala Tyr His Gly Asp Thr Val Gly Ala Val Ser
 145 150 155 160

480

GTA GGG GGT ATA GAA CTC TTC CAC GGA ACT TAT AAA GAT CTC CTT TTC
 Val Gly Gly Ile Glu Leu Phe His Gly Thr Tyr Lys Asp Leu Leu Phe
 165 170 175

528

AAG ACT ATA AAA CTC CCA TCT CCT TAC CTG TAC TGC AAG GAA AAG TAC Lys Thr Ile Lys Leu Pro Ser Pro Tyr Leu Tyr Cys Lys Glu Lys Tyr 180 185 190	576
GGG GAA CTC TGC CCT GAG TGC ACG GCA GAT TTA TTA AAA CAA CTG GAA Gly Glu Leu Cys Pro Glu Cys Thr Ala Asp Leu Leu Lys Gln Leu Glu 195 200 205	624
GAT ATC CTG AAG TCG CGG GAA GAT ATC GTT GCG GTC ATT ATG GAA GCG Asp Ile Leu Lys Ser Arg Glu Asp Ile Val Ala Val Ile Met Glu Ala 210 215 220	672
GGA ATT CAG GCA GCC GCG GGA ATG CTC CCC TTC CCT CCG GGA TTT TTG Gly Ile Gln Ala Ala Ala Gly Met Leu Pro Phe Pro Pro Gly Phe Leu 225 230 235 240	720
AAA GGC GTA AGG GAG CTT ACG AAG AAA TAC GAC ACT TTA ATG ATA GTT Lys Gly Val Arg Glu Leu Thr Lys Lys Tyr Asp Thr Leu Met Ile Val 245 250 255	768
GAC GAG GTT GCC ACG GGA TTT GGC AGG ACG GGA ACG ATG TTT TAC TGT Asp Glu Val Ala Thr Gly Phe Gly Arg Thr Gly Thr Met Phe Tyr Cys 260 265 270	816
GAG CAG GAA GGA GTC AGT CCG GAC TTT ATG TGT CTA GGT AAG GGT ATA Glu Gln Glu Gly Val Ser Pro Asp Phe Met Cys Leu Gly Lys Gly Ile 275 280 285	864
ACC GGA GGG TAC CTC CCG CTT GCT GCG ACA CTC ACA ACG GAC GAG GTG Thr Gly Gly Tyr Leu Pro Leu Ala Ala Thr Leu Thr Thr Asp Glu Val 290 295 300	912
TTC AAT GCC TTT TTA GGT GAG TTC GGG GAG GCA AAG CAC TTT TAC CAC Phe Asn Ala Phe Leu Glu Phe Gly Glu Ala Lys His Phe Tyr His 305 310 315 320	960
GGG CAC ACC TAC ACT GGA AAT AAC CTC GCC TGT TCC GTT GCA CTC GCA Gly His Thr Tyr Thr Gly Asn Asn Leu Ala Cys Ser Val Ala Leu Ala 325 330 335	1008
AAC TTA GAA GTT TTT GAG GAA GAA AGA ACT TTA GAG AAG CTC CAA CCA Asn Leu Glu Val Phe Glu Glu Glu Arg Thr Leu Glu Lys Leu Gln Pro 340 345 350	1056
AAG ATA AAG CTT TTA AAG GAA AGG CTT CAG GAG TTC TGG GAA CTC AAG Lys Ile Lys Leu Leu Lys Glu Arg Leu Gln Glu Phe Trp Glu Leu Lys 355 360 365	1104
CAC GTT GGA GAT GTT AGA CAG CTA GGT TTT ATG GCT GGA ATA GAG CTG His Val Gly Asp Val Arg Gln Leu Gly Phe Met Ala Gly Ile Glu Leu 370 375 380	1152
GTG AAG GAC AAA GAA AAG GGA GAA CCT TTC CCT TAC GGT GAA AGG ACG Val Lys Asp Lys Glu Lys Gly Glu Pro Phe Pro Tyr Gly Glu Arg Thr 385 390 395 400	1200
GGA TTT AAG GTG GCT TAC AAG TGC AGG GAA AAA GGG GTG TTT TTG AGA Gly Phe Lys Val Ala Tyr Lys Cys Arg Glu Lys Gly Val Phe Leu Arg 405 410 415	1245
CCG CTC GGA GAC GTT ATG GTA TTG ATG ATG CCT CTT GTA ATA GAG GAA Pro Leu Gly Asp Val Met Val Leu Met Met Pro Leu Val Ile Glu Glu	1293

420 425 430

GAC GAA ATG AAC TAC GTT ATT GAT ACA CTT AAA TGG GCA ATT AAA GAG 1341
 Asp Glu Met Asn Tyr Val Ile Asp Thr Leu Lys Trp Ala Ile Lys Glu
 435 440 445

CTT GAA AAA GAG GTG TAG 1359
 Leu Glu Lys Glu Val End
 450

(2) INFORMATION FOR SEQ ID NO:20:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1032 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG ACA TAC TTA ATG AAC AAT TAC GCA AGG TTG CCC GTA AAG TTT GTA 48
 Met Thr Tyr Leu Met Asn Asn Tyr Ala Arg Leu Pro Val Lys Phe Val
 5 10 15

AGG GGA AAA GGT GTT TAC CTG TAC GAT GAG GAA GGA AAG GAG TAT CTT 96
 Arg Gly Lys Gly Val Tyr Leu Tyr Asp Glu Glu Gly Lys Glu Tyr Leu
 20 25 30

GAC TTT GTC TCC GGT ATA GGC GTC AAC TCC CTC GGT CAC GCT TAC CCA 144
 Asp Phe Val Ser Gly Ile Gly Val Asn Ser Leu Gly His Ala Tyr Pro
 35 40 45

AAA CTC ACA GAA GCT CTA AAA GAA CAG GTT GAG AAA CTC CTC CAC GTT 192
 Lys Leu Thr Glu Ala Leu Lys Glu Gln Val Glu Lys Leu Leu His Val
 50 55 60

TCA AAT CTT TAC GAA AAC CCG TGG CAG GAA GAA CTG GCT CAC AAA CTT 240
 Ser Asn Leu Tyr Glu Asn Pro Trp Gln Glu Glu Leu Ala His Lys Leu
 65 70 75 80

GTA AAA CAC TTC TGG ACA GAA GGG AAG GTA TTT TTC GCA AAC AGC GGA 288
 Val Lys His Phe Thr Glu Gly Lys Val Phe Phe Ala Asn Ser Gly
 85 90 95

ACG GAA AGT GTA GAG GCG GCT ATA AAG CTC GCA AGG AAG TAC TGG AGG 336
 Thr Glu Ser Val Glu Ala Ala Ile Lys Leu Ala Arg Lys Tyr Trp Arg
 100 105 110

GAT AAA GGA AAG AAC AAG TGG AAG TTT ATA TCC TTT GAA AAC TCT TTC 384
 Asp Lys Gly Lys Asn Lys Trp Lys Phe Ile Ser Phe Glu Asn Ser Phe
 115 120 125

CAC GGG AGA ACC TAC GGT AGC CTC TCC GCA ACG GGA CAG CCA AAG TTC 432
 His Gly Arg Thr Tyr Gly Ser Leu Ser Ala Thr Gly Gln Pro Lys Phe
 130 135 140

CAC AAA GGC TTT GAA CCT CTA GTT CCT GGA TTT TCT TAC GCA AAG CTG 480
 His Lys Gly Phe Glu Pro Leu Val Pro Gly Phe Ser Tyr Ala Lys Leu
 145 150 155 160

AAC GAT ATA GAC AGC GTT TAC AAA CTC CTA GAC GAG GAA ACC GCG GGG 528

Asn Asp Ile Asp Ser Val Tyr Lys Leu Leu Asp Glu Glu Thr Ala Gly	165	170	175	
ATA ATT ATT GAA GTT ATA CAA GGA GAG GGC GGA GTA AAC GAG GCG AGT				576
Ile Ile Ile Glu Val Ile Gln Gly Glu Gly Gly Val Asn Glu Ala Ser	180	185	190	
GAG GAT TTT CTA AGT AAA CTC CAG GAA ATT TGT AAA GAA AAA GAT GTG				624
Glu Asp Phe Leu Ser Lys Leu Gln Glu Ile Cys Lys Glu Lys Asp Val	195	200	205	
CTC TTA ATT ATA GAC GAA GTG CAA ACG GGA ATA GGA AGG ACC GGG GAA				672
Leu Leu Ile Ile Asp Glu Val Gln Thr Gly Ile Gly Arg Thr Gly Glu	210	215	220	
TTC TAC GCA TAT CAA CAC TTC AAT CTA AAA CCG GAC GTA ATT GCG CTT				720
Phe Tyr Ala Tyr Gln His Phe Asn Leu Lys Pro Asp Val Ile Ala Leu	225	230	235	
GCG AAG GGA CTC GGA GGA GGT GTG CCA ATA GGT GCC ATC CTT GCA AGG				768
Ala Lys Gly Leu Gly Gly Gly Val Pro Ile Gly Ala Ile Leu Ala Arg	245	250	255	
GAA GAA GTG GCC CAG AGC TTT ACT CCC GGC TCC CAC GGC TCT ACC TTC				816
Glu Glu Val Ala Gln Ser Phe Thr Pro Gly Ser His Gly Ser Thr Phe	260	265	270	
GGA GGA AAC CCC TTA GCC TGC AGG GCG GGA ACA GTG GTA GTA GAT GAA				864
Gly Gly Asn Pro Leu Ala Cys Arg Ala Gly Thr Val Val Val Asp Glu	275	280	285	
GTT GAA AAA CTC CTG CCT CAC GTA AGG GAA GTG GGG AAT TAC TTC AAA				912
Val Glu Lys Leu Leu Pro His Val Arg Glu Val Gly Asn Tyr Phe Lys	290	295	300	
GAA AAA CTG AAG GAA CTC GGC AAA GGA AAG GTA AAG GGA AGA GGA TTG				960
Glu Lys Leu Lys Glu Leu Gly Lys Gly Lys Val Lys Gly Arg Gly Leu	305	310	315	
ATG CTC GGT CTT GAA CTT GAA AGA GAG TGT AAA GAT TAC GTT CTC AAG				1008
Met Leu Gly Leu Glu Leu Glu Arg Glu Cys Lys Asp Tyr Val Leu Lys	325	330	335	
GCT CTT GAA AGG GAC TTC TCA TAA				1032
Ala Leu Glu Arg Asp Phe Ser End	340			

- (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1197 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG CGG AAA CTG GCC GAG CGG GCG CAG AAA CTG AGC CCC TCT CCC ACC	48
Met Arg Lys Leu Ala Glu Arg Ala Gln Lys Leu Ser Pro Ser Pro Thr	
5 10 15	

CTC TCG GTG GAC ACC AAG GCC AAG GAG CTT TTG CGG CAG GGG GAA AGG Leu Ser Val Asp Thr Lys Ala Lys Glu Leu Leu Arg Gln Gly Glu Arg 20 25 30	96
GTC ATC AAT TTC GGG GCG GGG GAG CCG GAC TTC GAT ACA CCG GAA CAC Val Ile Asn Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Glu His 35 40 45	144
ATC AAG GAA GCG GCG AAG CGA GCT TTA GAT CAG GGC TTC ACC AAG TAC Ile Lys Glu Ala Ala Lys Arg Ala Leu Asp Gln Gly Phe Thr Lys Tyr 50 55 60	192
ACG CCG GTG GCT GGG ATC TTA CCT CTT CGG GAG GCC ATA TGC GAG AAG Thr Pro Val Ala Gly Ile Leu Pro Leu Arg Glu Ala Ile Cys Glu Lys 65 70 75 80	240
CTT TAC CGC GAC AAT CAA CTG GAA TAC AGC CCG AAT GAG ATC GTG GTC Leu Tyr Arg Asp Asn Gln Leu Glu Tyr Ser Pro Asn Glu Ile Val Val 85 90 95	288
TCC TGT GGC GCC AAG CAT TCT ATT TTC AAC GCT CTG CAG GTC CTC CTG Ser Cys Gly Ala Lys His Ser Ile Phe Asn Ala Leu Gln Val Leu Leu 100 105 110	336
GAC CCG GGG GAC GAG GTG ATA ATC CCC GTC CCC TAC TGG ACT TCC TAT Asp Pro Gly Asp Glu Val Ile Ile Pro Val Pro Tyr Trp Thr Ser Tyr 115 120 125	384
CCG GAG CAG GTG AAG CTG GCG GGA GGG GTG CCG GTT TTC GTC CCC ACC Pro Glu Gln Val Lys Leu Ala Gly Gly Val Pro Val Phe Val Pro Thr 130 135 140	432
TCT CCC GAG AAC GAC TTC AAG CTC AGG CCG GAA GAT CTA CGT GCG GCT Ser Pro Glu Asn Asp Phe Lys Leu Arg Pro Glu Asp Leu Arg Ala Ala 145 150 155 160	480
GTA ACC CCG CGC ACC CGC CTT TTG ATC CTC AAT TCC CCG GCC AAC CCC Val Thr Pro Arg Thr Arg Leu Leu Ile Leu Asn Ser Pro Ala Asn Pro 165 170 175	528
ACA GGC ACC GTT TAC CGC CGG GAG GAA CTT ATC GGC TTA GCG GAG GTA Thr Gly Thr Val Tyr Arg Arg Glu Glu Leu Ile Gly Leu Ala Glu Val 180 185 190	576
GCC CTG GAG GCC GAC CTA TGG ATC TTG TCG GAC GAG ATC TAC GAA AAG Ala Leu Glu Ala Asp Leu Trp Ile Leu Ser Asp Glu Ile Tyr Glu Lys 195 200 205	624
CTG ATC TAC GAC GGG ATG GAG CAC GTG AGC ATA GCC GCG CTC GAC CCG Leu Ile Tyr Asp Gly Met Glu His Val Ser Ile Ala Ala Leu Asp Pro 210 215 220	672
GAG GTC AAA AAG CGC ACG ATT GTG GTA AAC GGT GTT TCC AAG GCT TAC Glu Val Lys Lys Arg Thr Ile Val Val Asn Gly Val Ser Lys Ala Tyr 225 230 235 240	720
GCC ATG ACC GGT TGG CGC ATA GGT TAT GCT GCC GCT CCC CGG CCG ATA Ala Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Ala Pro Arg Pro Ile 245 250 255	768
GCC CAG GCC ATG ACC AAC CTC CAA AGC CAC AGT ACC TCT AAC CCC ACT Ala Gln Ala Met Thr Asn Leu Gln Ser His Ser Thr Ser Asn Pro Thr	816

260	265	270	
TCC GTA GCC CAG GCG GCG GCG CTG GCC GCT CTG AAG GGG CCA CAA GAG Ser Val Ala Gln Ala Ala Ala Leu Ala Ala Leu Lys Gly Pro Gln Glu 275 280 285			864
CCG GTG GAG AAC ATG CGC CGG GCT TTT CAA AAG CGG CGG GAT TTC ATC Pro Val Glu Asn Met Arg Arg Ala Phe Gln Lys Arg Arg Asp Phe Ile 290 295 300			912
TGG CAG TAC CTA AAC TCC TTA CCC GGA GTG CGC TGC CCC AAA CCT TTA Trp Gln Tyr Leu Asn Ser Leu Pro Gly Val Arg Cys Pro Lys Pro Leu 305 310 315 320			960
GGG GCC TTT TAC GTC TTT CCA GAA GTT GAG CGG GCT TTT GGG CCG CCG Gly Ala Phe Tyr Val Phe Pro Glu Val Glu Arg Ala Phe Gly Pro Pro 325 330 335			1008
TCT AAA AGG ACG GGA AAT ACT ACC GCT AGC GAC CTG GCC CTT TTC CTC Ser Lys Arg Thr Gly Asn Thr Thr Ala Ser Asp Leu Ala Leu Phe Leu 340 345 350			1056
CTG GAA GAG ATA AAA GTG GCC ACC GTG GCT GGG GCT GCC TTT GGG GAC Leu Glu Glu Ile Lys Val Ala Thr Val Ala Gly Ala Ala Phe Gly Asp 355 360 365			1104
GAT CGC TAC CTG CGC TTT TCC TAC GCC CTG CGG CTG GAA GAT ATC GAA Asp Arg Tyr Leu Arg Phe Ser Tyr Ala Leu Arg Leu Glu Asp Ile Glu 370 375 380			1152
GAG GGG ATG CAA CGG TTT AAA GAA TTG ATC GAA GCG GCA CTT TAA Glu Gly Met Gln Arg Phe Lys Glu Leu Ile Glu Ala Ala Leu End 385 390 395			1197

- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1779 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: GENOMIC DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG TGC GGG ATA GTC GGA TAC GTA GGG AGG GAT TTA GCC CTT CCT ATA Met Cys Gly Ile Val Gly Tyr Val Gly Arg Asp Leu Ala Leu Pro Ile 5 10 15	48
GTC CTC GGA GCT CTT GAG AGA CTC GAA TAC AGG GGT TAC GAC TCC GCG Val Leu Gly Ala Leu Glu Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala 20 25 30	96
GGA GTT GCC CTT ATA GAA GAC GGG AAA CTC ATA GTT GAA AAG AAG AAG Gly Val Ala Leu Ile Glu Asp Gly Lys Leu Ile Val Glu Lys Lys Lys 35 40 45	144
GGA AAG ATA AGG GAA CTC GTT AAA GCG CTA TGG GGA AAG GAT TAC AAG Gly Lys Ile Arg Glu Leu Val Lys Ala Leu Trp Gly Lys Asp Tyr Lys 50 55 60	192

GCT AAA ACG GGT ATA GGT CAC ACA CGC TGG GCA ACC CAC GGA AAG CCC Ala Lys Thr Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Lys Pro 65 70 75 80	240
ACG GAC GAG AAC GCC CAC CCC CAC ACC GAC GAA AAA GGT GAG TTT GCA Thr Asp Glu Asn Ala His Pro His Thr Asp Glu Lys Gly Glu Phe Ala 85 90 95	288
GTA GTT CAC AAC GGG ATA ATA GAA AAC TAC TTA GAA CTA AAA GAG GAA Val Val His Asn Gly Ile Ile Glu Asn Tyr Leu Glu Leu Lys Glu Glu 100 105 110	336
CTA AAG AAG GAA GGT GTA AAG TTC AGG TCC GAA ACA GAC ACA GAA GTT Leu Lys Lys Glu Gly Val Lys Phe Arg Ser Glu Thr Asp Thr Glu Val 115 120 125	384
ATA GCC CAC CTC ATA GCG AAG AAC TAC AGG GGG GAC TTA CTG GAG GCC Ile Ala His Leu Ile Ala Lys Asn Tyr Arg Gly Asp Leu Leu Glu Ala 130 135 140	432
GTT TTA AAA ACC GTA AAG AAA TTA AAG GGT GCT TTT GCC TTT GCG GTT Val Leu Lys Thr Val Lys Lys Leu Lys Gly Ala Phe Ala Phe Ala Val 145 150 155 160	480
ATA ACG GTT CAC GAA CCA AAC AGA CTA ATA GGA GTG AAG CAG GGG AGT Ile Thr Val His Glu Pro Asn Arg Leu Ile Gly Val Lys Gln Gly Ser 165 170 175	528
CCT TTA ATC GTC GGA CTC GGA GAA GGA GAA AAC TTC CTC GCT TCA GAT Pro Leu Ile Val Gly Leu Gly Glu Gly Glu Asn Phe Leu Ala Ser Asp 180 185 190	576
ATT CCC GCA ATA CTT CCT TAC ACG AAA AAG ATT ATT GTT CTT GAT GAC Ile Pro Ala Ile Leu Pro Tyr Thr Lys Lys Ile Ile Val Leu Asp Asp 195 200 205	624
GGG GAA ATA GCG GAC CTG ACT CCC GAC ACT GTG AAC ATT TAC AAC TTT Gly Glu Ile Ala Asp Leu Thr Pro Asp Thr Val Asn Ile Tyr Asn Phe 210 215 220	672
GAG GGA GAG CCC GTT TCA AAG GAA GTA ATG ATT ACG CCC TGG GAT CTT Glu Gly Glu Pro Val Ser Lys Glu Val Met Ile Thr Pro Trp Asp Leu 225 230 235 240	720
GTT TCT GCG GAA AAG GGT GGT TTT AAA CAC TTC ATG CTA AAA GAG ATA Val Ser Ala Glu Lys Gly Gly Phe Lys His Phe Met Leu Lys Glu Ile 245 250 255	768
TAC GAA CAG CCC AAA GCC ATA AAC GAC ACA CTC AAG GGT TTC CTC TCA Tyr Glu Gln Pro Lys Ala Ile Asn Asp Thr Leu Lys Gly Phe Leu Ser 260 265 270	816
ACC GAA GAC GCA ATA CCC TTT AAG TTA AAA GAC TTC AGA AGG GTT TTA Thr Glu Asp Ala Ile Pro Phe Lys Leu Lys Asp Phe Arg Arg Val Leu 275 280 285	864
ATA ATA GCG TGC GGG ACC TCT TAC CAC GCG GGC TTC GTC GGA AAG TAC Ile Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Phe Val Gly Lys Tyr 290 295 300	912
TGG ATA GAG AGA TTT GCA GGT GTT CCC ACA GAG GTA ATT TAC GCT TCG Trp Ile Glu Arg Phe Ala Gly Val Pro Thr Glu Val Ile Tyr Ala Ser	960

305		310		315		320	
GAA TTC AGG TAT GCG GAC GTT CCC GTT TCG GAC AAG GAT ATC GTT ATC							1008
Glu Phe Arg Tyr Ala Asp Val Pro Val Ser Asp Lys Asp Ile Val Ile							
		325		330		335	
GGA ATT TCC CAG TCA GGA GAG ACC GCT GAC ACA AAG TTT GCC CTT CAG							1056
Gly Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Lys Phe Ala Leu Gln							
		340		345		350	
TCC GCA AAG GAA AAG GGA GCC TTT ACC GTG GGA CTC GTA AAC GTA GTG							1104
Ser Ala Lys Glu Lys Gly Ala Phe Thr Val Gly Leu Val Asn Val Val							
		355		360		365	
GGA AGT GCC ATA GAC AGG GAG TCG GAC TTT TCC CTT CAC ACA CAT GCG							1152
Gly Ser Ala Ile Asp Arg Glu Ser Asp Phe Ser Leu His Thr His Ala							
		370		375		380	
GGA CCC GAA ATA GGC GTG GCG GCT ACA AAG ACC TTC ACC GCA CAG TTC							1200
Gly Pro Glu Ile Gly Val Ala Ala Thr Lys Thr Phe Thr Ala Gln Phe							
		385		390		395	
ACC GCA CTC TAC GCC CTT TCG GTA AGG GAA AGT GAG GAG AGG GAA AAT							1248
Thr Ala Leu Tyr Ala Leu Ser Val Arg Glu Ser Glu Glu Arg Glu Asn							
		405		410		415	
CTA ATA AGA CTC CTT GAA AAG GTT CCA TCA CTC GTT GAA CAA ACA CTG							1296
Leu Ile Arg Leu Leu Glu Lys Val Pro Ser Leu Val Glu Gln Thr Leu							
		420		425		430	
AAC ACC GCA GAA GAA GTG GAG AAG GTA GCG GAA AAG TAC ATG AAA AAG							1344
Asn Thr Ala Glu Glu Val Glu Lys Val Ala Glu Lys Tyr Met Lys Lys							
		435		440		445	
AAA AAC ATG CTT TAC CTC GGA AGG TAC TTA AAT TAC CCC ATA GCG CTG							1392
Lys Asn Met Leu Tyr Leu Gly Arg Tyr Leu Asn Tyr Pro Ile Ala Leu							
		450		455		460	
GAG GGA GCT CTT AAA CTT AAA GAA ATT TCT TAC ATA CAC GCG GAA GGT							1440
Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Gly							
		465		470		475	
TAT CCC GCA GGG GAG ATG AAG CAC GGT CCC ATA GCC CTC ATA GAC GAA							1488
Tyr Pro Ala Gly Glu Met Lys His Gly Pro Ile Ala Leu Ile Asp Glu							
		485		490		495	
AAC ATG CCG GTT GTG GTA ATC GCA CCG AAA GAC AGG GTT TAC GAG AAG							1536
Asn Met Pro Val Val Val Ile Ala Pro Lys Asp Arg Val Tyr Glu Lys							
		500		505		510	
ATA CTC TCA AAC GTA GAA GAG GTT CTC GCA AGA AAG GGA AGG GTT ATT							1584
Ile Leu Ser Asn Val Glu Glu Val Leu Ala Arg Lys Gly Arg Val Ile							
		515		520		525	
TCT GTA GGC TTT AAA GGA GAC GAA ACT CTC AAA AGC AAA TCC GAG AGC							1632
Ser Val Gly Phe Lys Gly Asp Glu Thr Leu Lys Ser Lys Ser Glu Ser							
		530		535		540	
GTT ATG GAA ATC CCG AAG GCA GAA GAA CCG ATA ACT CCT TTC TTG ACG							1680
Val Met Glu Ile Pro Lys Ala Glu Glu Pro Ile Thr Pro Phe Leu Thr							
		545		550		555	
GTA ATA CCC CTG CAA CTC TTT GCC TAC TTT ATA GCG AGC AAA CTG GGA							1728
Val Ile Pro Leu Gln Leu Phe Ala Tyr Phe Ile Ala Ser Lys Leu Gly							

565 570 575 580

CTG GAT GTG GAT CAG CCG AGA AAT CTC GCC AAA ACG GTC ACG GTG GAA 1776
 Leu Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Thr Val Thr Val Glu
 580 585 590

TAA
 End

- (2) INFORMATION FOR SEQ ID NO:23:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1065 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG ATA CCC CAG AGG ATT AAG GAA CTT GAA GCT TAC AAG ACG GAG GTC 48
 Met Ile Pro Gln Arg Ile Lys Glu Leu Glu Ala Tyr Lys Thr Glu Val
 5 10 15

ACT CCC GCC TCC GTC AGG CTT TCC TCT AAC GAA TTC CCC TAC GAC TTT 96
 Thr Pro Ala Ser Val Arg Leu Ser Ser Asn Glu Phe Pro Tyr Asp Phe
 20 25 30

CCC GAG GAG ATA AAA CAA AGG GCC TTA GAA GAA TTA AAA AAG GTT CCC 144
 Pro Glu Glu Ile Lys Gln Arg Ala Leu Glu Glu Leu Lys Lys Val Pro
 35 40 45

TTG AAC AAA TAC CCA GAC CCC GAA GCG AAA GAG TTA AAA GCG GTT CTT 192
 Leu Asn Lys Tyr Pro Asp Pro Glu Ala Lys Glu Leu Lys Ala Val Leu
 50 55 60

GCG GAT TTT TTC GGC GTT AAG GAA GAA AAT TTA GTT CTC GGT AAC GGT 240
 Ala Asp Phe Phe Gly Val Lys Glu Glu Asn Leu Val Leu Gly Asn Gly
 65 70 75 80

TCG GAC GAA CTC ATA TAC TAC CTC TCA ATA GCT ATA GGT GAA CTT TAC 288
 Ser Asp Glu Leu Ile Tyr Tyr Leu Ser Ile Ala Ile Gly Glu Leu Tyr
 85 90 95

ATA CCC GTT TAC ATA CCT GTT CCC ACC TTT CCC ATG TAC GAG ATA AGT 336
 Ile Pro Val Tyr Ile Pro Val Pro Thr Phe Pro Met Tyr Glu Ile Ser
 100 105 110

GCG AAA GTT CTC GGA AGA CCC CTC GTA AAG GTT CAA CTG GAC GAA AAC 384
 Ala Lys Val Leu Gly Arg Pro Leu Val Lys Val Gln Leu Asp Glu Asn
 115 120 125

TTT GAT ATA GAC TTA GAA AGA AGT ATT GAA TTA ATA GAG AAA GAA AAA 432
 Phe Asp Ile Asp Leu Glu Arg Ser Ile Glu Leu Ile Glu Lys Glu Lys
 130 135 140

CCC GTT CTC GGG TAC TTT GCT TAC CCA AAC AAC CCC ACG GGA AAC CTC 480
 Pro Val Leu Gly Tyr Phe Ala Tyr Pro Asn Asn Pro Thr Gly Asn Leu
 145 150 155 160

TTT TCC AGG GGA AAG ATT GAG GAG ATA AGA AAC AGG GGT GTT TTC TGT 528
 Phe Ser Arg Gly Lys Ile Glu Glu Ile Arg Asn Arg Gly Val Phe Cys

165	170	175	
GTA ATA GAC GAA GCC TAC TAT CAT TAC TCC GGA GAA ACC TTT CTG GAA Val Ile Asp Glu Ala Tyr Tyr His Tyr Ser Gly Glu Thr Phe Leu Glu 180 185 190			576
GAC GCG CTC AAA AGG GAA GAT ACG GTA GTT TTG AGG ACA CTT TCA AAA Asp Ala Leu Lys Arg Glu Asp Thr Val Val Leu Arg Thr Leu Ser Lys 195 200 205			624
ATC GGT ATG GCG AGT TTA AGG GTA GGG ATT TTA ATA GGG AAG GGG GAA Ile Gly Met Ala Ser Leu Arg Val Gly Ile Leu Ile Gly Lys Gly Glu 210 215 220			672
ATC GTC TCA GAA ATT AAC AAG GTG AGA CTC CCC TTC AAC GTG ACC TAC Ile Val Ser Glu Ile Asn Lys Val Arg Leu Pro Phe Asn Val Thr Tyr 225 230 235 240			720
CCC TCT CAG GTG ATG GCA AAA GTT CTC CTC ACG GAG GGA AGA GAA TTC Pro Ser Gln Val Met Ala Lys Val Leu Thr Glu Gly Arg Glu Phe 245 250 255			768
CTA ATG GAA AAG ATA CAG GAG GTT GTA ACA GAG CGA GAA AGG ATG TAC Leu Met Glu Lys Ile Gln Glu Val Val Thr Glu Arg Glu Arg Met Tyr 260 265 270			816
GAC GAA ATG AAG AAA ATA GAA GGA GTT GAG GTT TTT CCG AGT AAG GCT Asp Glu Met Lys Lys Ile Glu Gly Val Glu Val Phe Pro Ser Lys Ala 275 280 285			864
AAC TTC TTG CTT TTC AGA ACG CCT TAC CCC GCC CAC GAG GTT TAT CAG Asn Phe Leu Leu Phe Arg Thr Pro Tyr Pro Ala His Glu Val Tyr Gln 290 295 300			912
GAG CTA CTG AAA AGG GAT GTC CTC GTC AGG AAC GTA TCT TAC ATG GAA Glu Leu Leu Lys Arg Asp Val Leu Val Arg Asn Val Ser Tyr Met Glu 305 310 315 320			960
GGA CTC CAA AAG TGC CTC AGG GTA AGC GTA GGG AAA CCG GAA GAA AAC Gly Leu Gln Lys Cys Leu Arg Val Ser Val Gly Lys Pro Glu Glu Asn 325 330 335			1008
AAC AAG TTT CTG GAA GCA CTG GAG GAG AGT ATA AAA TCC CTT TCA AGC Asn Lys Phe Leu Glu Ala Leu Glu Glu Ser Ile Lys Ser Leu Ser Ser 340 345 350			1056
TCT CTT TAA Ser Leu End			1065

- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 912 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG AAG CCG TAC GCT AAA TAT ATC TGG CTT GAC GGC AGA ATA CTT AAG

48

Met Lys Pro Tyr Ala Lys Tyr Ile Trp Leu Asp Gly Arg Ile Leu Lys
5 10 15

TGG GAA GAC GCG AAA ATA CAC GTG TTG ACT CAC GCG CTT CAC TAC GGA 96
Trp Glu Asp Ala Lys Ile His Val Leu Thr His Ala Leu His Tyr Gly
20 25 30

ACC TCT ATA TTC GAG GGA ATA AGA GGG TAT TGG AAC GGC GAT AAT TTG 144
Thr Ser Ile Phe Glu Gly Ile Arg Gly Tyr Trp Asn Gly Asp Asn Leu
35 40 45

CTC GTC TTT AGG TTA GAA GAA CAC ATC GAC CGC ATG TAC AGA TCG GCT 192
Leu Val Phe Arg Leu Glu Glu His Ile Asp Arg Met Tyr Arg Ser Ala
50 55 60

AAG ATA CTA GGC ATA AAT ATT CCG TAT ACA AGA GAG GAA GTC CGC CAA 240
Lys Ile Leu Gly Ile Asn Ile Pro Tyr Thr Arg Glu Glu Val Arg Gln
65 70 75 80

GCT GTA CTA GAG ACC ATA AAG GCT AAT AAC TTC CGA GAG GAT GTC TAC 288
Ala Val Leu Glu Thr Ile Lys Ala Asn Asn Phe Arg Glu Asp Val Tyr
85 90 95

ATA AGA CCT GTG GCG TTT GTC GCC TCG CAG ACG GTG ACG CTT GAC ATA 336
Ile Arg Pro Val Ala Phe Val Ala Ser Gln Thr Val Thr Leu Asp Ile
100 105 110

AGA AAT TTG GAA GTC TCC CTC GCG GTT ATT GTA TTC CCA TTT GGC AAA 384
Arg Asn Leu Glu Val Ser Leu Ala Val Ile Val Phe Pro Phe Gly Lys
115 120 125

TAC CTC TCG CCC AAC GGC ATT AAG GCA ACG ATT GTA AGC TGG CGT AGA 432
Tyr Leu Ser Pro Asn Gly Ile Lys Ala Thr Ile Val Ser Trp Arg Arg
130 135 140

GTA CAT AAT ACA ATG CTC CCT GTG ATG GCA AAA ATC GGC GGT ATA TAT 480
Val His Asn Thr Met Leu Pro Val Met Ala Lys Ile Gly Gly Ile Tyr
145 150 155 160

GTA AAC TCT GTA CTT GCG CTT GTA GAG GCT AGA AGC AGG GGA TTT GAC 528
Val Asn Ser Val Leu Ala Leu Val Glu Ala Arg Ser Arg Gly Phe Asp
165 170 175

GAG GCT TTA TTA ATG GAC GTT AAC GGT TAT GTT GTT GAG GGT TCT GGA 576
Glu Ala Leu Leu Met Asp Val Asn Gly Tyr Val Val Glu Gly Ser Gly
180 185 190

GAG AAT ATT TTC ATT GTC AGA GGT GGA AGG CTT TTC ACG CCG CCA GTA 624
Glu Asn Ile Phe Ile Val Arg Gly Gly Arg Leu Phe Thr Pro Pro Val
195 200 205

CAC GAA TCT ATC CTC GAG GGA ATT ACG AGG GAT ACG GTA ATA AAG CTC 672
His Glu Ser Ile Leu Glu Gly Ile Thr Arg Asp Thr Val Ile Lys Leu
210 215 220

AGC GGG GAT GTG GGA CTT CGG GTG GAG GAA AAG CCT ATT ACG AGG GAG 720
Ser Gly Asp Val Gly Leu Arg Val Glu Glu Lys Pro Ile Thr Arg Glu
225 230 235 240

GAG GTG TAT ACA GCC GAC GAG GTG TTT TTA GTA GGA ACC GCC GCA GAG 768
Glu Val Tyr Thr Ala Asp Glu Val Phe Leu Val Gly Thr Ala Ala Glu
245 250 255

ATA ACG CCA GTG GTG GAG GTT GAC GGC AGA ACA ATC GGC ACA GGC AAG 816
 Ile Thr Pro Val Val Glu Val Asp Gly Arg Thr Ile Gly Thr Gly Lys
 260 265 270

CCG GGC CCC ATT ACG ACA AAA ATA GCT GAG CTG TAC TCA AAC GTC GTG 864
 Pro Gly Pro Ile Thr Thr Lys Ile Ala Glu Leu Tyr Ser Asn Val Val
 275 280 285

AGA GGC AAA GTA GAG AAA TAC TTA AAT TGG ATC ACT CCT GTG TAT TAG 912

Arg Gly Lys Val Glu Lys Tyr Leu Asn Trp Ile Thr Pro Val Tyr End
 290 295 300

- (2) INFORMATION FOR SEQ ID NO:25:
- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 414 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ile Glu Asp Pro Met Asp Trp Ala Phe Pro Arg Ile Lys Arg Leu
 5 10 15

Pro Gln Tyr Val Phe Ser Leu Val Asn Glu Leu Lys Tyr Lys Leu Arg
 20 25 30

Arg Glu Gly Glu Asp Val Val Asp Leu Gly Met Gly Asn Pro Asn Met
 35 40 45

Pro Pro Ala Lys His Ile Ile Asp Lys Leu Cys Glu Val Ala Gln Lys
 50 55 60

Pro Asn Val His Gly Tyr Ser Ala Ser Arg Gly Ile Pro Arg Leu Arg
 65 70 75 80

Lys Ala Ile Cys Asn Phe Tyr Glu Glu Arg Tyr Gly Val Lys Leu Asp
 85 90 95

Pro Glu Arg Glu Ala Ile Leu Thr Ile Gly Ala Lys Glu Gly Tyr Ser
 100 105 110

His Leu Met Leu Ala Met Ile Ser Pro Gly Asp Thr Val Ile Val Pro
 115 120 125

Asn Pro Thr Tyr Pro Ile His Tyr Tyr Ala Pro Ile Ile Ala Gly Gly
 130 135 140

Glu Val His Ser Ile Pro Leu Asn Phe Ser Asp Asp Gln Asp His Gln
 145 150 155 160

Glu Glu Phe Leu Arg Arg Leu Tyr Glu Ile Val Lys Thr Ala Met Pro
 165 170 175

Lys Pro Lys Ala Val Val Ile Ser Phe Pro His Asn Pro Thr Thr Ile
 180 185 190

Thr Val Glu Lys Asp Phe Phe Lys Glu Ile Val Lys Phe Ala Lys Glu
 195 200 205

His Gly Leu Trp Ile Ile His Asp Phe Ala Tyr Ala Asp Ile Ala Phe
 210 215 220
 Asp Gly Tyr Lys Pro Pro Ser Ile Leu Glu Ile Glu Gly Ala Lys Asp
 225 230 235 240
 Val Ala Val Glu Leu Tyr Ser Met Ser Lys Gly Phe Ser Met Ala Gly
 245 250 255
 Trp Arg Val Ala Phe Val Val Gly Asn Glu Ile Leu Ile Lys Asn Leu
 260 265 270
 Ala His Leu Lys Ser Tyr Leu Asp Tyr Gly Ile Phe Thr Pro Ile Gln
 275 280 285
 Val Ala Ser Ile Ile Ala Leu Glu Ser Pro Tyr Glu Ile Val Glu Lys
 290 295 300
 Thr Ala Lys Val Tyr Gln Lys Arg Arg Asp Val Leu Val Glu Gly Leu
 305 310 315 320
 Asn Arg Leu Gly Trp Lys Val Lys Lys Pro Lys Ala Thr Met Phe Val
 325 330 335
 Trp Ala Lys Ile Pro Glu Trp Ile Asn Met Asn Ser Leu Asp Phe Ser
 340 345 350
 Leu Phe Leu Leu Lys Glu Ala Lys Val Ala Val Ser Pro Gly Val Gly
 355 360 365
 Phe Gly Gln Tyr Gly Glu Gly Tyr Val Arg Phe Ala Leu Val Glu Asn
 370 375 380
 Glu His Arg Ile Arg Gln Ala Ile Arg Gly Ile Arg Lys Ala Phe Arg
 385 390 395 400
 Lys Leu Gln Lys Glu Arg Lys Leu Glu Pro Glu Arg Ser Ala End
 405 410 414

- (2) INFORMATION FOR SEQ ID NO:26:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 373 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asp Arg Leu Glu Lys Val Ser Pro Phe Ile Val Met Asp Ile Leu
 5 10 15
 Ala Gln Ala Gln Lys Tyr Glu Asp Val Val His Met Glu Ile Gly Glu
 20 25 30
 Pro Asp Leu Glu Pro Ser Pro Lys Val Met Glu Ala Leu Glu Arg Ala
 35 40 45
 Val Lys Glu Lys Thr Phe Phe Tyr Thr Pro Ala Leu Gly Leu Trp Glu
 50 55 60
 Leu Arg Glu Arg Ile Ser Glu Phe Tyr Arg Lys Lys Tyr Ser Val Glu

- (2) INFORMATION FOR SEQ ID NO:27:
- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 453 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Trp Glu Leu Asp Pro Lys Thr Leu Glu Lys Trp Asp Lys Glu Tyr
 5 10 15

Phe Trp His Pro Phe Thr Gln Met Lys Val Tyr Arg Glu Glu Asn
 20 25 30

Leu Ile Phe Glu Arg Gly Glu Gly Val Tyr Leu Trp Asp Ile Tyr Gly
 35 40 45

Arg Lys Tyr Ile Asp Ala Ile Ser Ser Leu Trp Cys Asn Val His Gly
 50 55 60

His Asn His Pro Lys Leu Asn Asn Ala Val Met Lys Gln Leu Cys Lys
 65 70 75 80

Val Ala His Thr Thr Thr Leu Gly Ser Ser Asn Val Pro Ala Ile Leu
 85 90 95

Leu Ala Lys Lys Leu Val Glu Ile Ser Pro Glu Gly Leu Asn Lys Val
 100 105 110

Phe Tyr Ser Glu Asp Gly Ala Glu Ala Val Glu Ile Ala Ile Lys Met
 115 120 125

Ala Tyr His Tyr Trp Lys Asn Lys Gly Val Lys Gly Lys Asn Val Phe
 130 135 140

Ile Thr Leu Ser Glu Ala Tyr His Gly Asp Thr Val Gly Ala Val Ser
 145 150 155 160

Val Gly Gly Ile Glu Leu Phe His Gly Thr Tyr Lys Asp Leu Leu Phe
 165 170 175

Lys Thr Ile Lys Leu Pro Ser Pro Tyr Leu Tyr Cys Lys Glu Lys Tyr
 180 185 190

Gly Glu Leu Cys Pro Glu Cys Thr Ala Asp Leu Leu Lys Gln Leu Glu
 195 200 205

Asp Ile Leu Lys Ser Arg Glu Asp Ile Val Ala Val Ile Met Glu Ala
 210 215 220

Gly Ile Gln Ala Ala Ala Gly Met Leu Pro Phe Pro Pro Gly Phe Leu
 225 230 235 240

Lys Gly Val Arg Glu Leu Thr Lys Lys Tyr Asp Thr Leu Met Ile Val
 245 250 255

Asp Glu Val Ala Thr Gly Phe Gly Arg Thr Gly Thr Met Phe Tyr Cys
 260 265 270

Glu Gln Glu Gly Val Ser Pro Asp Phe Met Cys Leu Gly Lys Gly Ile
 275 280 285
 Thr Gly Gly Tyr Leu Pro Leu Ala Ala Thr Leu Thr Thr Asp Glu Val
 290 295 300
 Phe Asn Ala Phe Leu Gly Glu Phe Gly Glu Ala Lys His Phe Tyr His
 305 310 315 320
 Gly His Thr Tyr Thr Gly Asn Asn Leu Ala Cys Ser Val Ala Leu Ala
 325 330 335
 Asn Leu Glu Val Phe Glu Glu Glu Arg Thr Leu Glu Lys Leu Gln Pro
 340 345 350
 Lys Ile Lys Leu Leu Lys Glu Arg Leu Gln Glu Phe Trp Glu Leu Lys
 355 360 365
 His Val Gly Asp Val Arg Gln Leu Gly Phe Met Ala Gly Ile Glu Leu
 370 375 380
 Val Lys Asp Lys Glu Lys Gly Glu Pro Phe Pro Tyr Gly Glu Arg Thr
 385 390 395 400
 Gly Phe Lys Val Ala Tyr Lys Cys Arg Glu Lys Gly Val Phe Leu Arg
 405 410 415
 Pro Leu Gly Asp Val Met Val Leu Met Met Pro Leu Val Ile Glu Glu
 420 425 430
 Asp Glu Met Asn Tyr Val Ile Asp Thr Leu Lys Trp Ala Ile Lys Glu
 435 440 445
 Leu Glu Lys Glu Val
 450

- (2) INFORMATION FOR SEQ ID NO:28:
- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 343 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Thr Tyr Leu Met Asn Asn Tyr Ala Arg Leu Pro Val Lys Phe Val
 5 10 15
 Arg Gly Lys Gly Val Tyr Leu Tyr Asp Glu Glu Gly Lys Glu Tyr Leu
 20 25 30
 Asp Phe Val Ser Gly Ile Gly Val Asn Ser Leu Gly His Ala Tyr Pro
 35 40 45
 Lys Leu Thr Glu Ala Leu Lys Glu Gln Val Glu Lys Leu Leu His Val
 50 55 60
 Ser Asn Leu Tyr Glu Asn Pro Trp Gln Glu Glu Leu Ala His Lys Leu
 65 70 75 80

Val Lys His Phe Trp Thr Glu Gly Lys Val Phe Phe Ala Asn Ser Gly
 85 90 95
 Thr Glu Ser Val Glu Ala Ala Ile Lys Leu Ala Arg Lys Tyr Trp Arg
 100 105 110
 Asp Lys Gly Lys Asn Lys Trp Lys Phe Ile Ser Phe Glu Asn Ser Phe
 115 120 125
 His Gly Arg Thr Tyr Gly Ser Leu Ser Ala Thr Gly Gln Pro Lys Phe
 130 135 140
 His Lys Gly Phe Glu Pro Leu Val Pro Gly Phe Ser Tyr Ala Lys Leu
 145 150 155 160
 Asn Asp Ile Asp Ser Val Tyr Lys Leu Leu Asp Glu Glu Thr Ala Gly
 165 170 175
 Ile Ile Ile Glu Val Ile Gln Gly Glu Gly Gly Val Asn Glu Ala Ser
 180 185 190
 Glu Asp Phe Leu Ser Lys Leu Gln Glu Ile Cys Lys Glu Lys Asp Val
 195 200 205
 Leu Leu Ile Ile Asp Glu Val Gln Thr Gly Ile Gly Arg Thr Gly Glu
 210 215 220
 Phe Tyr Ala Tyr Gln His Phe Asn Leu Lys Pro Asp Val Ile Ala Leu
 225 230 235 240
 Ala Lys Gly Leu Gly Gly Gly Val Pro Ile Gly Ala Ile Leu Ala Arg
 245 250 255
 Glu Glu Val Ala Gln Ser Phe Thr Pro Gly Ser His Gly Ser Thr Phe
 260 265 270
 Gly Gly Asn Pro Leu Ala Cys Arg Ala Gly Thr Val Val Val Asp Glu
 275 280 285
 Val Glu Lys Leu Leu Pro His Val Arg Glu Val Gly Asn Tyr Phe Lys
 290 295 300
 Glu Lys Leu Lys Glu Leu Gly Lys Gly Lys Val Lys Gly Arg Gly Leu
 305 310 315 320
 Met Leu Gly Leu Glu Leu Glu Arg Glu Cys Lys Asp Tyr Val Leu Lys
 325 330 335
 Ala Leu Glu Arg Asp Phe Ser
 340

- (2) INFORMATION FOR SEQ ID NO:29:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 398 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Arg Lys Leu Ala Glu Arg Ala Gln Lys Leu Ser Pro Ser Pro Thr
5 10 15
Leu Ser Val Asp Thr Lys Ala Lys Glu Leu Leu Arg Gln Gly Glu Arg
20 25 30
Val Ile Asn Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Glu His
35 40 45
Ile Lys Glu Ala Ala Lys Arg Ala Leu Asp Gln Gly Phe Thr Lys Tyr
50 55 60
Thr Pro Val Ala Gly Ile Leu Pro Leu Arg Glu Ala Ile Cys Glu Lys
65 70 75 80
Leu Tyr Arg Asp Asn Gln Leu Glu Tyr Ser Pro Asn Glu Ile Val Val
85 90 95
Ser Cys Gly Ala Lys His Ser Ile Phe Asn Ala Leu Gln Val Leu Leu
100 105 110
Asp Pro Gly Asp Glu Val Ile Ile Pro Val Pro Tyr Trp Thr Ser Tyr
115 120 125
Pro Glu Gln Val Lys Leu Ala Gly Gly Val Pro Val Phe Val Pro Thr
130 135 140
Ser Pro Glu Asn Asp Phe Lys Leu Arg Pro Glu Asp Leu Arg Ala Ala
145 150 155 160
Val Thr Pro Arg Thr Arg Leu Leu Ile Leu Asn Ser Pro Ala Asn Pro
165 170 175
Thr Gly Thr Val Tyr Arg Arg Glu Glu Leu Ile Gly Leu Ala Glu Val
180 185 190
Ala Leu Glu Ala Asp Leu Trp Ile Leu Ser Asp Glu Ile Tyr Glu Lys
195 200 205
Leu Ile Tyr Asp Gly Met Glu His Val Ser Ile Ala Ala Leu Asp Pro
210 215 220
Glu Val Lys Lys Arg Thr Ile Val Val Asn Gly Val Ser Lys Ala Tyr
225 230 235 240
Ala Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Ala Pro Arg Pro Ile
245 250 255
Ala Gln Ala Met Thr Asn Leu Gln Ser His Ser Thr Ser Asn Pro Thr
260 265 270
Ser Val Ala Gln Ala Ala Ala Leu Ala Ala Leu Lys Gly Pro Gln Glu
275 280 285
Pro Val Glu Asn Met Arg Arg Ala Phe Gln Lys Arg Arg Asp Phe Ile
290 295 300
Trp Gln Tyr Leu Asn Ser Leu Pro Gly Val Arg Cys Pro Lys Pro Leu
305 310 315 320

Gly Ala Phe Tyr Val Phe Pro Glu Val Glu Arg Ala Phe Gly Pro Pro
325 330 335

Ser Lys Arg Thr Gly Asn Thr Thr Ala Ser Asp Leu Ala Leu Phe Leu
340 345 350

Leu Glu Glu Ile Lys Val Ala Thr Val Ala Gly Ala Ala Phe Gly Asp
355 360 365

Asp Arg Tyr Leu Arg Phe Ser Tyr Ala Leu Arg Leu Glu Asp Ile Glu
370 375 380

Glu Gly Met Gln Arg Phe Lys Glu Leu Ile Glu Ala Ala Leu
385 390 395

- (2) INFORMATION FOR SEQ ID NO:30:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 592 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Cys Gly Ile Val Gly Tyr Val Gly Arg Asp Leu Ala Leu Pro Ile
5 10 15

Val Leu Gly Ala Leu Glu Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

Gly Val Ala Leu Ile Glu Asp Gly Lys Leu Ile Val Glu Lys Lys Lys
35 40 45

Gly Lys Ile Arg Glu Leu Val Lys Ala Leu Trp Gly Lys Asp Tyr Lys
50 55 60

Ala Lys Thr Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Lys Pro
65 70 75 80

Thr Asp Glu Asn Ala His Pro His Thr Asp Glu Lys Gly Glu Phe Ala
85 90 95

Val Val His Asn Gly Ile Ile Glu Asn Tyr Leu Glu Leu Lys Glu Glu
100 105 110

Leu Lys Lys Glu Gly Val Lys Phe Arg Ser Glu Thr Asp Thr Glu Val
115 120 125

Ile Ala His Leu Ile Ala Lys Asn Tyr Arg Gly Asp Leu Leu Glu Ala
130 135 140

Val Leu Lys Thr Val Lys Lys Leu Lys Gly Ala Phe Ala Phe Ala Val
145 150 155 160

Ile Thr Val His Glu Pro Asn Arg Leu Ile Gly Val Lys Gln Gly Ser
165 170 175

Pro Leu Ile Val Gly Leu Gly Glu Gly Glu Asn Phe Leu Ala Ser Asp
180 185 190

Ile Pro Ala Ile Leu Pro Tyr Thr Lys Lys Ile Ile Val Leu Asp Asp
 195 200 205
 Gly Glu Ile Ala Asp Leu Thr Pro Asp Thr Val Asn Ile Tyr Asn Phe
 210 215 220
 Glu Gly Glu Pro Val Ser Lys Glu Val Met Ile Thr Pro Trp Asp Leu
 225 230 235 240
 Val Ser Ala Glu Lys Gly Gly Phe Lys His Phe Met Leu Lys Glu Ile
 245 250 255
 Tyr Glu Gln Pro Lys Ala Ile Asn Asp Thr Leu Lys Gly Phe Leu Ser
 260 265 270
 Thr Glu Asp Ala Ile Pro Phe Lys Leu Lys Asp Phe Arg Arg Val Leu
 275 280 285
 Ile Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Phe Val Gly Lys Tyr
 290 295 300
 Trp Ile Glu Arg Phe Ala Gly Val Pro Thr Glu Val Ile Tyr Ala Ser
 305 310 315 320
 Glu Phe Arg Tyr Ala Asp Val Pro Val Ser Asp Lys Asp Ile Val Ile
 325 330 335
 Gly Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Lys Phe Ala Leu Gln
 340 345 350
 Ser Ala Lys Glu Lys Gly Ala Phe Thr Val Gly Leu Val Asn Val Val
 355 360 365
 Gly Ser Ala Ile Asp Arg Glu Ser Asp Phe Ser Leu His Thr His Ala
 370 375 380
 Gly Pro Glu Ile Gly Val Ala Ala Thr Lys Thr Phe Thr Ala Gln Phe
 385 390 395 400
 Thr Ala Leu Tyr Ala Leu Ser Val Arg Glu Ser Glu Glu Arg Glu Asn
 405 410 415
 Leu Ile Arg Leu Leu Glu Lys Val Pro Ser Leu Val Glu Gln Thr Leu
 420 425 430
 Asn Thr Ala Glu Glu Val Glu Lys Val Ala Glu Lys Tyr Met Lys Lys
 435 440 445
 Lys Asn Met Leu Tyr Leu Gly Arg Tyr Leu Asn Tyr Pro Ile Ala Leu
 450 455 460
 Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Gly
 465 470 475 480
 Tyr Pro Ala Gly Glu Met Lys His Gly Pro Ile Ala Leu Ile Asp Glu
 485 490 495
 Asn Met Pro Val Val Val Ile Ala Pro Lys Asp Arg Val Tyr Glu Lys
 500 505 510
 Ile Leu Ser Asn Val Glu Glu Val Leu Ala Arg Lys Gly Arg Val Ile
 515 520 525

Ser Val Gly Phe Lys Gly Asp Glu Thr Leu Lys Ser Lys Ser Glu Ser
530 535 540

Val Met Glu Ile Pro Lys Ala Glu Glu Pro Ile Thr Pro Phe Leu Thr
545 550 555 560

Val Ile Pro Leu Gln Leu Phe Ala Tyr Phe Ile Ala Ser Lys Leu Gly
565 570 575

Leu Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Thr Val Thr Val Glu
580 585 590

- (2) INFORMATION FOR SEQ ID NO:31:
- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 354 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Ile Pro Gln Arg Ile Lys Glu Leu Glu Ala Tyr Lys Thr Glu Val
5 10 15

Thr Pro Ala Ser Val Arg Leu Ser Ser Asn Glu Phe Pro Tyr Asp Phe
20 25 30

Pro Glu Glu Ile Lys Gln Arg Ala Leu Glu Glu Leu Lys Lys Val Pro
35 40 45

Leu Asn Lys Tyr Pro Asp Pro Glu Ala Lys Glu Leu Lys Ala Val Leu
50 55 60

Ala Asp Phe Phe Gly Val Lys Glu Glu Asn Leu Val Leu Gly Asn Gly
65 70 75 80

Ser Asp Glu Leu Ile Tyr Tyr Leu Ser Ile Ala Ile Gly Glu Leu Tyr
85 90 95

Ile Pro Val Tyr Ile Pro Val Pro Thr Phe Pro Met Tyr Glu Ile Ser
100 105 110

Ala Lys Val Leu Gly Arg Pro Leu Val Lys Val Gln Leu Asp Glu Asn
115 120 125

Phe Asp Ile Asp Leu Glu Arg Ser Ile Glu Leu Ile Glu Lys Glu Lys
130 135 140

Pro Val Leu Gly Tyr Phe Ala Tyr Pro Asn Asn Pro Thr Gly Asn Leu
145 150 155 160

Phe Ser Arg Gly Lys Ile Glu Glu Ile Arg Asn Arg Gly Val Phe Cys
165 170 175

Val Ile Asp Glu Ala Tyr Tyr His Tyr Ser Gly Glu Thr Phe Leu Glu
180 185 190

Asp Ala Leu Lys Arg Glu Asp Thr Val Val Leu Arg Thr Leu Ser Lys
195 200 205

Ile Gly Met Ala Ser Leu Arg Val Gly Ile Leu Ile Gly Lys Gly Glu
 210 215 220

Ile Val Ser Glu Ile Asn Lys Val Arg Leu Pro Phe Asn Val Thr Tyr
 225 230 235 240

Pro Ser Gln Val Met Ala Lys Val Leu Leu Thr Glu Gly Arg Glu Phe
 245 250 255

Leu Met Glu Lys Ile Gln Glu Val Val Thr Glu Arg Glu Arg Met Tyr
 260 265 270

Asp Glu Met Lys Lys Ile Glu Gly Val Glu Val Phe Pro Ser Lys Ala
 275 280 285

Asn Phe Leu Leu Phe Arg Thr Pro Tyr Pro Ala His Glu Val Tyr Gln
 290 295 300

Glu Leu Leu Lys Arg Asp Val Leu Val Arg Asn Val Ser Tyr Met Glu
 305 310 315 320

Gly Leu Gln Lys Cys Leu Arg Val Ser Val Gly Lys Pro Glu Glu Asn
 325 330 335

Asn Lys Phe Leu Glu Ala Leu Glu Glu Ser Ile Lys Ser Leu Ser Ser
 340 345 350

Ser Leu

- (2) INFORMATION FOR SEQ ID NO:32:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 303 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Lys Pro Tyr Ala Lys Tyr Ile Trp Leu Asp Gly Arg Ile Leu Lys
 5 10 15

Trp Glu Asp Ala Lys Ile His Val Leu Thr His Ala Leu His Tyr Gly
 20 25 30

Thr Ser Ile Phe Glu Gly Ile Arg Gly Tyr Trp Asn Gly Asp Asn Leu
 35 40 45

Leu Val Phe Arg Leu Glu Glu His Ile Asp Arg Met Tyr Arg Ser Ala
 50 55 60

Lys Ile Leu Gly Ile Asn Ile Pro Tyr Thr Arg Glu Glu Val Arg Gln
 65 70 75 80

Ala Val Leu Glu Thr Ile Lys Ala Asn Asn Phe Arg Glu Asp Val Tyr
 85 90 95

Ile Arg Pro Val Ala Phe Val Ala Ser Gln Thr Val Thr Leu Asp Ile
 100 105 110

Arg Asn Leu Glu Val Ser Leu Ala Val Ile Val Phe Pro Phe Gly Lys
115 120 125

Tyr Leu Ser Pro Asn Gly Ile Lys Ala Thr Ile Val Ser Trp Arg Arg
130 135 140

Val His Asn Thr Met Leu Pro Val Met Ala Lys Ile Gly Gly Ile Tyr
145 150 155 160

Val Asn Ser Val Leu Ala Leu Val Glu Ala Arg Ser Arg Gly Phe Asp
165 170 175

Glu Ala Leu Leu Met Asp Val Asn Gly Tyr Val Val Glu Gly Ser Gly
180 185 190

Glu Asn Ile Phe Ile Val Arg Gly Gly Arg Leu Phe Thr Pro Pro Val
195 200 205

His Glu Ser Ile Leu Glu Gly Ile Thr Arg Asp Thr Val Ile Lys Leu
210 215 220

Ser Gly Asp Val Gly Leu Arg Val Glu Glu Lys Pro Ile Thr Arg Glu
225 230 235 240

Glu Val Tyr Thr Ala Asp Glu Val Phe Leu Val Gly Thr Ala Ala Glu
245 250 255

Ile Thr Pro Val Val Glu Val Asp Gly Arg Thr Ile Gly Thr Gly Lys
260 265 270

Pro Gly Pro Ile Thr Thr Lys Ile Ala Glu Leu Tyr Ser Asn Val Val
275 280 285

Arg Gly Lys Val Glu Lys Tyr Leu Asn Trp Ile Thr Pro Val Tyr
290 295 300

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGGCAGTC AAAGTGCGGC CT

52

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGGAGGATCC TTATCCAAAG CTTCCAGGAA G

31

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 1,092 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATG GCA GTC AAA GTG CGG CCT GAG CTC AGC CAG GTG GAG ATC TAC CGT	48
Met Ala Val Lys Val Arg Pro Glu Leu Ser Gln Val Glu Ile Tyr Arg	
5 10 15	
CCC GGC AAA CCC ATC GAA GAG GTA AAG AAG GAG CTG GGG CTG GAG GAG	96
Pro Gly Lys Pro Ile Glu Glu Val Lys Lys Glu Leu Gly Leu Glu Glu	
20 25 30	
GTA GTC AAG CTG GCC TCC AAC GAG AAC CCT CTG GGA CCT TCT CCC AAG	144
Val Val Lys Leu Ala Ser Asn Glu Asn Pro Leu Gly Pro Ser Pro Lys	
35 40 45	
GCC GTG GCG GCG CTG GAG GGA CTG GAC CAC TGG CAC CTT TAC CCA GAA	192
Ala Val Ala Ala Leu Glu Gly Leu Asp His Trp His Leu Tyr Pro Glu	
50 55 60	
GGC TCA AGC TAT GAG CTA CGG GCG CTG GGT AAG AAA CTG GAG ATA	240
Gly Ser Ser Tyr Glu Leu Arg Gln Ala Leu Gly Lys Lys Leu Glu Ile	
65 70 75 80	
GAC CCG GAC AGC ATC ATC GTG GGT TGC GGC TCA AGC GAA GTC ATC CAG	288
Asp Pro Asp Ser Ile Ile Val Gly Cys Gly Ser Ser Glu Val Ile Gln	
85 90 95	
ATG CTC TCT TTG GCC CTG CTG GCG CCC GGC GAC GAG GTG GTC ATC CCT	336
Met Leu Ser Leu Ala Leu Leu Ala Pro Gly Asp Glu Val Val Ile Pro	
100 105 110	
GTG CCT ACC TTT CCC CGC TAT GAG CCC CTG GCA CGG CTC ATG GGG GCT	384
Val Pro Thr Phe Pro Arg Tyr Glu Pro Leu Ala Arg Leu Met Gly Ala	
115 120 125	
AAT CCC GTA AAA GTT CCC TTG AAG GAC TAC CGC ATC GAT GTG GAG GCA	432
Asn Pro Val Lys Val Pro Leu Lys Asp Tyr Arg Ile Asp Val Glu Ala	
130 135 140	
GTG GCC CGA GCC CTT TCC CCC CGT ACC AAG CTG GTC TAC CTA TGC AAC	480
Val Ala Arg Ala Leu Ser Pro Arg Thr Lys Leu Val Tyr Leu Cys Asn	
145 150 155 160	
CCC AAC AAC CCC ACC GGG ACC ATC GTC ACC CGG GAG GAG GTG GAG TGG	528
Pro Asn Asn Pro Thr Gly Thr Ile Val Thr Arg Glu Glu Val Glu Trp	
165 170 175	

TTC TTG GAA AAG GCG GGG GAG GGG GTT CTC ACC GTG CTG GAC GAG GCC Phe Leu Glu Lys Ala Gly Glu Gly Val Leu Thr Val Leu Asp Glu Ala 180 185 190	576
TAC TGC GAG TAC GTG ACC AGC CCC GCC TAC CCT GAT GGG CTC GAT TTC Tyr Cys Glu Tyr Val Thr Ser Pro Ala Tyr Pro Asp Gly Leu Asp Phe 195 200 205	624
CTG CGC CGG GGC TAC AAT GTG GTG GTG CTG CGC ACC TTC TCC AAG ATC Leu Arg Arg Gly Tyr Asn Val Val Val Leu Arg Thr Phe Ser Lys Ile 210 215 220	672
TAC GGG CTG GCC GGG CTG CGC ATA GGG TAC GGT GTG GCG GAC AGG GAG Tyr Gly Leu Ala Gly Leu Arg Ile Gly Tyr Gly Val Ala Asp Arg Glu 225 230 235 240	720
CTG GTG GCG GAA CTG CAC CGG GTG CGG GAG CCT TTC AAT GTC AGT TCC Leu Val Ala Glu Leu His Arg Val Arg Glu Pro Phe Asn Val Ser Ser 245 250 255	768
GCT GCT CAG ATA GCC GCC CTG GCC GCC CTG GAA GAC GAA GAG TTC GTG Ala Ala Gln Ile Ala Ala Leu Ala Leu Glu Asp Glu Glu Phe Val 260 265 270	816
GCG CTT TCG CGC CAG GTC AAC GAA GAA GGG AAG GTT TTT CTC TAC CGA Ala Leu Ser Arg Gln Val Asn Glu Glu Gly Lys Val Phe Leu Tyr Arg 275 280 285	864
GAA CTG GAG AGG CGG GGG ATC GCC TAC GTG CCC ACC GAG GCC AAC TTC Glu Leu Glu Arg Arg Gly Ile Ala Tyr Val Pro Thr Glu Ala Asn Phe 290 295 300	912
CTA CTC TTC GAT GCC GGT CGG GAC GAG CAG GAA GTA TTT CGC CGG ATG Leu Leu Phe Asp Ala Gly Arg Asp Glu Gln Glu Val Phe Arg Arg Met 305 310 315 320	960
CTG CGC CAG GGA GTG ATC ATC CGG GNC GGG GTG GGT TAT CCC ACC CAC Leu Arg Gln Gly Val Ile Ile Arg Xxx Gly Val Gly Tyr Pro Thr His 325 330 335	1008
TTA AGG GTG ACC ATC GGC ACC TTG GAA CAG AAC CAG CGC TTC CTG GAA Leu Arg Val Thr Ile Gly Thr Leu Glu Gln Asn Gln Arg Phe Leu Glu 340 345 350	1056
GCT TTG GAT AAG GCT CTA GAG CTT AGG GGG GTT TAA Ala Leu Asp Lys Ala Leu Glu Leu Arg Gly Val 355 360 363	1092

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: AMINO ACIDS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Val Lys Val Arg Pro Glu Leu Ser Gln Val Glu Ile Tyr Arg
5 10 15

Pro Gly Lys Pro Ile Glu Glu Val Lys Lys Glu Leu Gly Leu Glu Glu

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGGAGGATCC TTAGATCTCT TCAAGGGCTT T

31

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 1,085 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATG AGA AAA GGA CTT GCA AGT AGG GTA AGT CAC CTA AAA CCT TCC CCC	48
Met Arg Lys Gly Leu Ala Ser Arg Val Ser His Leu Lys Pro Ser Pro	
5 10 15	
ACG CTG ACC ATA ACC GCA AAA GCA AAA GAA TTA AGG GCT AAA GGA GTG	96
Thr Leu Thr Ile Thr Ala Lys Ala Lys Glu Leu Arg Ala Lys Gly Val	
20 25 30	
GAC GTT ATA GGT TTT GGA GCG GGA GAA CCT GAC TTC GAC ACA CCC GAC	144
Asp Val Ile Gly Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Asp	
35 40 45	
TTC ATA AAG GAA GCC TGT ATA AGG GCT TTA AGG GAA GGA AAG ACC AAG	192
Phe Ile Lys Glu Ala Cys Ile Arg Ala Leu Arg Glu Gly Lys Thr Lys	
50 55 60	
TAC GCT CCC TCC GCG GGA ATA CCA GAG CTC AGA GAA GCT ATA GCT GAA	240
Tyr Ala Pro Ser Ala Gly Ile Pro Glu Leu Arg Glu Ala Ile Ala Glu	
65 70 75 80	
AAA CTA CTG AAA GAA AAC AAA GTT GAG TAC AAA CCT TCA GAG ATA GTC	288
Lys Leu Leu Lys Glu Asn Lys Val Glu Tyr Lys Pro Ser Glu Ile Val	
85 90 95	
GTT TCC GCA GGA GCG AAA ATG GTT CTC TTC CTC ATA TTC ATG GCT ATA	336
Val Ser Ala Gly Ala Lys Met Val Leu Phe Leu Ile Phe Met Ala Ile	
100 105 110	
CTG GAC GAA GGA GAC GAG GTT TTA CTA CCT AGC CCT TAC TGG GTA ACT	384
Leu Asp Glu Gly Asp Glu Val Leu Leu Pro Ser Pro Tyr Trp Val Thr	
115 120 125	
TAC CCC GAA CAG ATA AGG TTC TTC GGA GGG GTT CCC GTT GAG GTT CCT	432
Tyr Pro Glu Gln Ile Arg Phe Phe Gly Gly Val Pro Val Glu Val Pro	
130 135 140	
CTA AAG AAA GAG AAA GGA TTT CAA TTA AGT CTG GAA GAT GTG AAA GAA	480
Leu Lys Lys Glu Lys Gly Phe Gln Leu Ser Leu Glu Asp Val Lys Glu	
145 150 155 160	

GCG CTT TCG CGC CAG GTC AAC GAA GAA GGG AAG GTT TTT CTC TAC CGA	864
Ala Leu Ser Arg Gln Val Asn Glu Glu Gly Lys Val Phe Leu Tyr Arg	
275 280 285	
GAA CTG GAG AGG CGG GGG ATC GCC TAC GTG CCC ACC GAG GCC AAC TTC	912
Glu Leu Glu Arg Arg Gly Ile Ala Tyr Val Pro Thr Glu Ala Asn Phe	
290 295 300	
CTA CTC TTC GAT GCC GGT CGG GAC GAG CAG GAA GTA TTT CGC CGG ATG	960
Leu Leu Phe Asp Ala Gly Arg Asp Glu Gln Glu Val Phe Arg Arg Met	
305 310 315 320	
CTG CGC CAG GGA GTG ATC ATC CGG GNC GGG GTG GGT TAT CCC ACC CAC	1008
Leu Arg Gln Gly Val Ile Ile Arg Xxx Gly Val Gly Tyr Pro Thr His	
325 330 335	
TTA AGG GTG ACC ATC GGC ACC TTG GAA CAG AAC CAG CGC TTC CTG GAA	1056
Leu Arg Val Thr Ile Gly Thr Leu Glu Gln Asn Gln Arg Phe Leu Glu	
340 345 350	
GCT TTG GAT AAG GCT CTA GAG CTT AGG GGG GTT TAA	1092
Ala Leu Asp Lys Ala Leu Glu Leu Arg Gly Val	
355 360 363	

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: AMINO ACIDS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE-DESCRIPTION: SEQ ID NO:36:

Met Ala Val Lys Val Arg Pro Glu Leu Ser Gln Val Glu Ile Tyr Arg	15
5 10	
Pro Gly Lys Pro Ile Glu Glu Val Lys Lys Glu Leu Gly Leu Glu Glu	30
20 25	
Val Val Lys Leu Ala Ser Asn Glu Asn Pro Leu Gly Pro Ser Pro Lys	45
35 40	
Ala Val Ala Ala Leu Glu Gly Leu Asp His Trp His Leu Tyr Pro Glu	60
50 55	
Gly Ser Ser Tyr Glu Leu Arg Gln Ala Leu Gly Lys Lys Leu Glu Ile	80
65 70 75	
Asp Pro Asp Ser Ile Ile Val Gly Cys Gly Ser Ser Glu Val Ile Gln	95
85 90	
Met Leu Ser Leu Ala Leu Leu Ala Pro Gly Asp Glu Val Val Ile Pro	110
100 105	

Val Pro Thr Phe Pro Arg Tyr Glu Pro Leu Ala Arg Leu Met Gly Ala
 115 120 125
 Asn Pro Val Lys Val Pro Leu Lys Asp Tyr Arg Ile Asp Val Glu Ala
 130 135 140
 Val Ala Arg Ala Leu Ser Pro Arg Thr Lys Leu Val Tyr Leu Cys Asn
 145 150 155 160
 Pro Asn Asn Pro Thr Gly Thr Ile Val Thr Arg Glu Glu Val Glu Trp
 165 170 175
 Phe Leu Glu Lys Ala Gly Glu Gly Val Leu Thr Val Leu Asp Glu Ala
 180 185 190
 Tyr Cys Glu Tyr Val Thr Ser Pro Ala Tyr Pro Asp Gly Leu Asp Phe
 195 200 205
 Leu Arg Arg Gly Tyr Asn Val Val Val Leu Arg Thr Phe Ser Lys Ile
 210 215 220
 Tyr Gly Leu Ala Gly Leu Arg Ile Gly Tyr Gly Val Ala Asp Arg Glu
 225 230 235 240
 Leu Val Ala Glu Leu His Arg Val Arg Glu Pro Phe Asn Val Ser Ser
 245 250 255
 Ala Ala Gln Ile Ala Ala Leu Ala Ala Leu Glu Asp Glu Glu Phe Val
 260 265 270
 Ala Leu Ser Arg Gln Val Asn Glu Glu Gly Lys Val Phe Leu Tyr Arg
 275 280 285
 Glu Leu Glu Arg Arg Gly Ile Ala Tyr Val Pro Thr Glu Ala Asn Phe
 290 295 300
 Leu Leu Phe Asp Ala Gly Arg Asp Glu Gln Glu Val Phe Arg Arg Met
 305 310 315 320
 Leu Arg Gln Gly Val Ile Ile Arg Xxx Gly Val Gly Tyr Pro Thr His
 325 330 335
 Leu Arg Val Thr Ile Gly Thr Leu Glu Gln Asn Gln Arg Phe Leu Glu
 340 345 350
 Ala Leu Asp Lys Ala Leu Glu Leu Arg Gly Val
 355 360 363

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 52 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAGAAAA GGAATTGCAA GT
 52

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 31 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGGAGGATCC TTAGATCTCT TCAAGGGCTT T
 31

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1,085 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATG AGA AAA GGA CTT GCA AGT AGG GTA AGT CAC CTA AAA CCT TCC CC48
 Met Arg Lys Gly Leu Ala Ser Arg Val Ser His Leu Lys Pro Ser Pro
 5 10 15

ACG CTG ACC ATA ACC GCA AAA GCA AAA GAA TTA AGG GCT AAA GGA GT96
 Thr Leu Thr Ile Thr Ala Lys Ala Lys Glu Leu Arg Ala Lys Gly Val
 20 25 30

GAC GTT ATA GGT TTT GGA GCG GGA GAA CCT GAC TTC GAC ACA CCC GA44
 Asp Val Ile Gly Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Asp
 35 40 45

TTC ATA AAG GAA GCC TGT ATA AGG GCT TTA AGG GAA GGA AAG ACC AAC
Phe Ile Lys Glu Ala Cys Ile Arg Ala Leu Arg Glu Gly Lys Thr Lys
50 55 60

TAC GCT CCC TCC GCG GGA ATA CCA GAG CTC AGA GAA GCT ATA GCT GAA
Tyr Ala Pro Ser Ala Gly Ile Pro Glu Leu Arg Glu Ala Ile Ala Glu
65 70 75 80

AAA CTA CTG AAA GAA AAC AAA GTT GAG TAC AAA CCT TCA GAG ATA GAA
Lys Leu Leu Lys Glu Asn Lys Val Glu Tyr Lys Pro Ser Glu Ile Val
85 90 95

GTT TCC GCA GGA GCG AAA ATG GTT CTC TTC CTC ATA TTC ATG GCT AAA
Val Ser Ala Gly Ala Lys Met Val Leu Phe Leu Ile Phe Met Ala Ile
100 105 110

CTG GAC GAA GGA GAC GAG GTT TTA CTA CCT AGC CCT TAC TGG GTA AAG
Leu Asp Glu Gly Asp Glu Val Leu Leu Pro Ser Pro Tyr Trp Val Thr
115 120 125

TAC CCC GAA CAG ATA AGG TTC TTC GGA GGG GTT CCC GTT GAG GTT CAA
Tyr Pro Glu Gln Ile Arg Phe Phe Gly Gly Val Pro Val Glu Val Pro
130 135 140

CTA AAG AAA GAG AAA GGA TTT CAA TTA AGT CTG GAA GAT GTG AAA GAA
Leu Lys Lys Glu Lys Gly Phe Gln Leu Ser Leu Glu Asp Val Lys Glu
145 150 155 160

AAG GTT ACG GAG AGA ACA AAA GCT ATA GTC ATA AAC TCT CCG AAC AAG
Lys Val Thr Glu Arg Thr Lys Ala Ile Val Ile Asn Ser Pro Asn Asn
165 170 175

CCC ACT GGT GCT GTT TAC GAA GAG GAG GAA CTT AAG AAA ATA GCG GAA
Pro Thr Gly Ala Val Tyr Glu Glu Glu Glu Leu Lys Lys Ile Ala Glu
180 185 190

TTT TGC GTG GAG AGG GGC ATT TTC ATA ATT TCC GAT GAG TGC TAT GAA
Phe Cys Val Glu Arg Gly Ile Phe Ile Ile Ser Asp Glu Cys Tyr Glu
195 200 205

TAC TTC GTT TAC GGT GAT GCA AAA TTT GTT AGC CCT GCC TCT TTC TGG
Tyr Phe Val Tyr Gly Asp Ala Lys Phe Val Ser Pro Ala Ser Phe Ser
210 215 220

GAT GAA GTA AAG AAC ATA ACC TTC ACG GTA AAC GCC TTT TCG AAG AAG
Asp Glu Val Lys Asn Ile Thr Phe Thr Val Asn Ala Phe Ser Lys Ser
225 230 235 240

TAT TCC ATG ACT GGT TGG CGA ATA GGT TAT GTA GCG TGC CCC GAA GAA
Tyr Ser Met Thr Gly Trp Arg Ile Gly Tyr Val Ala Cys Pro Glu Glu
245 250 255

TAC GCA AAA GTG ATA GCG AGT CTT AAC AGC CAG AGT GTT TCC AAC GAA

Tyr Ala Lys Val Ile Ala Ser Leu Asn Ser Gln Ser Val Ser Asn Val
260 270

ACT ACC TTT GCC CAG TAT GGA GCT CTT GAG GCC TTG AAA AAT CCA AAG
Thr Thr Phe Ala Gln Tyr Gly Ala Leu Glu Ala Leu Lys Asn Pro Lys
275 280 285

TCT AAA GAT TTT GTA AAC GAA ATG AGA AAT GCT TTT GAA AGG AGA AAG
Ser Lys Asp Phe Val Asn Glu Met Arg Asn Ala Phe Glu Arg Arg Arg
290 295 300

GAT ACG GCT GTA GAA GAG CTT TCT AAA ATT CCA GGT ATG GAT GTG GAA
Asp Thr Ala Val Glu Leu Ser Lys Ile Pro Gly Met Asp Val Val
305 310 315 320

AAA CCC GAA GGT GCC TTT TAC ATA TTT CCG GAC TTC TCC GCT TAC GAA
Lys Pro Glu Gly Ala Phe Tyr Ile Phe Pro Asp Phe Ser Ala Tyr Ala
325 330 335

GAG AAA CTG GGT GGT GAT GTG AAA CTC TCG GAG TTC CTT CTG GAA AAG
Glu Lys Leu Gly Gly Asp Val Lys Leu Ser Glu Phe Leu Leu Glu Lys
340 345 350

GCT AAG GTT GCG GTG GTT CCC GGT TCG GCC TTC GGA GCT CCC GGA TTT
Ala Lys Val Ala Val Val Pro Gly Ser Ala Phe Gly Ala Pro Gly Phe
355 360 365

TTG AGG CTT TCT TAC GCC CTT TCC GAG GAA AGA CTC GTT GAG GGT ATA
Leu Arg Leu Ser Tyr Ala Leu Ser Glu Glu Arg Leu Val Glu Gly Ile
370 375 380 385

AGG AGA ATA AAG AAA GCC CTT GAA GAG ATC TAA
Arg Arg Ile Lys Lys Ala Leu Glu Glu Ile
385 390 394

1185

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 394 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Arg Lys Gly Leu Ala Ser Arg Val Ser His Leu Lys Pro Ser Pro
5 10 15

Thr Leu Thr Ile Thr Ala Lys Ala Lys Glu Leu Arg Ala Lys Gly Val

	20	25	30
Asp Val	Ile Gly Phe Gly Ala Gly	Glu Pro Asp Phe Asp Thr Pro Asp	
	35	40	45
Phe Ile	Lys Glu Ala Cys Ile Arg Ala Leu Arg Glu Gly Lys Thr Lys		
	50	55	60
Tyr Ala	Pro Ser Ala Gly Ile Pro Glu Leu Arg Glu Ala Ile Ala Glu		
	65	70	75
Lys Leu	Leu Lys Glu Asn Lys Val Glu Tyr Lys Pro Ser Glu Ile Val		
	85	90	95
Val Ser	Ala Gly Ala Lys Met Val Leu Phe Leu Ile Phe Met Ala Ile		
	100	105	110
Leu Asp	Glu Gly Asp Glu Val Leu Leu Pro Ser Pro Tyr Trp Val Thr		
	115	120	125
Tyr Pro	Glu Gln Ile Arg Phe Phe Gly Gly Val Pro Val Glu Val Pro		
	130	135	140
Leu Lys	Lys Glu Lys Gly Phe Gln Leu Ser Leu Glu Asp Val Lys Glu		
	145	150	155
Lys Val	Thr Glu Arg Thr Lys Ala Ile Val Ile Asn Ser Pro Asn Asn		
	165	170	175
Pro Thr	Gly Ala Val Tyr Glu Glu Glu Glu Leu Lys Lys Ile Ala Glu		
	180	185	190
Phe Cys	Val Glu Arg Gly Ile Phe Ile Ile Ser Asp Glu Cys Tyr Glu		
	195	200	205
Tyr Phe	Val Tyr Gly Asp Ala Lys Phe Val Ser Pro Ala Ser Phe Ser		
	210	215	220
Asp Glu	Val Lys Asn Ile Thr Phe Thr Val Asn Ala Phe Ser Lys Ser		
	225	230	235
Tyr Ser	Met Thr Gly Trp Arg Ile Gly Tyr Val Ala Cys Pro Glu Glu		
	245	250	255
Tyr Ala	Lys Val Ile Ala Ser Leu Asn Ser Gln Ser Val Ser Asn Val		
	260	265	270
Thr Thr	Phe Ala Gln Tyr Gly Ala Leu Glu Ala Leu Lys Asn Pro Lys		
	275	280	285
Ser Lys	Asp Phe Val Asn Glu Met Arg Asn Ala Phe Glu Arg Arg Arg		
	290	295	300

Asp Thr Ala Val Glu Glu Leu Ser Lys Ile Pro Gly Met Asp Val Val
305 310 315 320

Lys Pro Glu Gly Ala Phe Tyr Ile Phe Pro Asp Phe Ser Ala Tyr Ala
325 330 335

Glu Lys Leu Gly Gly Asp Val Lys Leu Ser Glu Phe Leu Leu Glu Lys
340 345 350

Ala Lys Val Ala Val Val Pro Gly Ser Ala Phe Gly Ala Pro Gly Phe
355 360 365

Leu Arg Leu Ser Tyr Ala Leu Ser Glu Glu Arg Leu Val Glu Gly Ile
370 375 380

Arg Arg Ile Lys Lys Ala Leu Glu Glu Ile
385 390 394

*See
C10
enclosed*